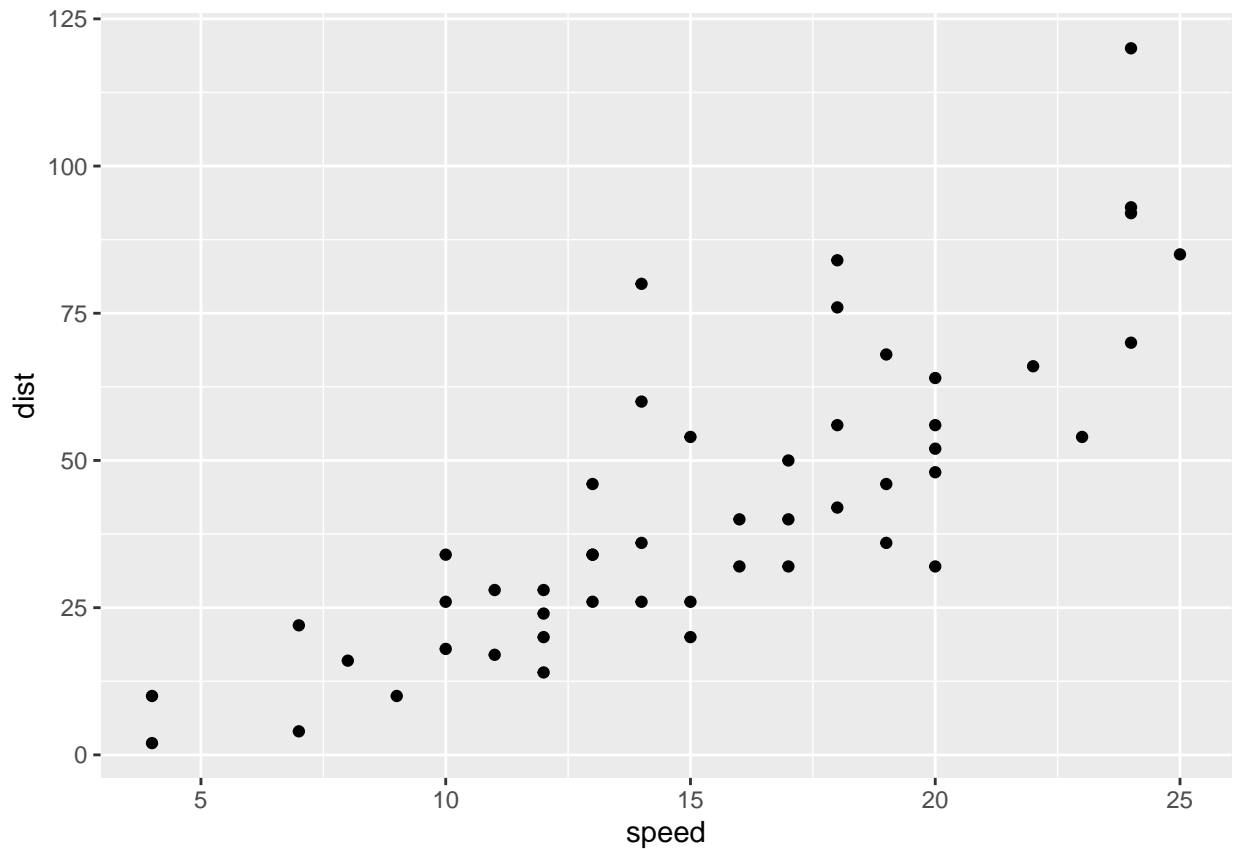


Class 05 Data Visualization

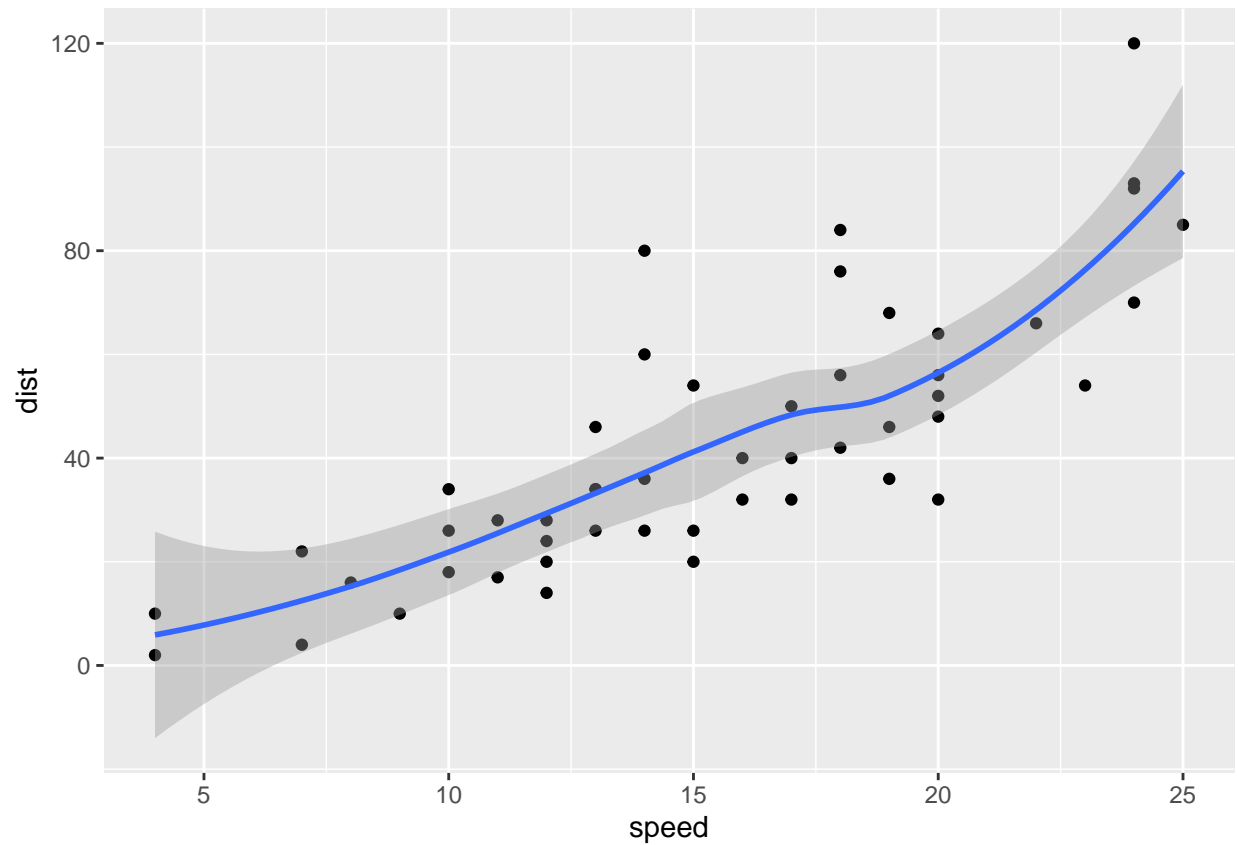
Hayoung Park (PID A15531571)

2021-10-12

```
#Class 05 Data Visualization  
  
#starting w/ a scatterplot  
#before we can use it, we have to load it up and make sure it is installed  
#install.packages("ggplot2")  
library(ggplot2)  
  
#try making a scatterplot  
ggplot(data=cars) + aes(x=speed, y=dist) + geom_point()
```

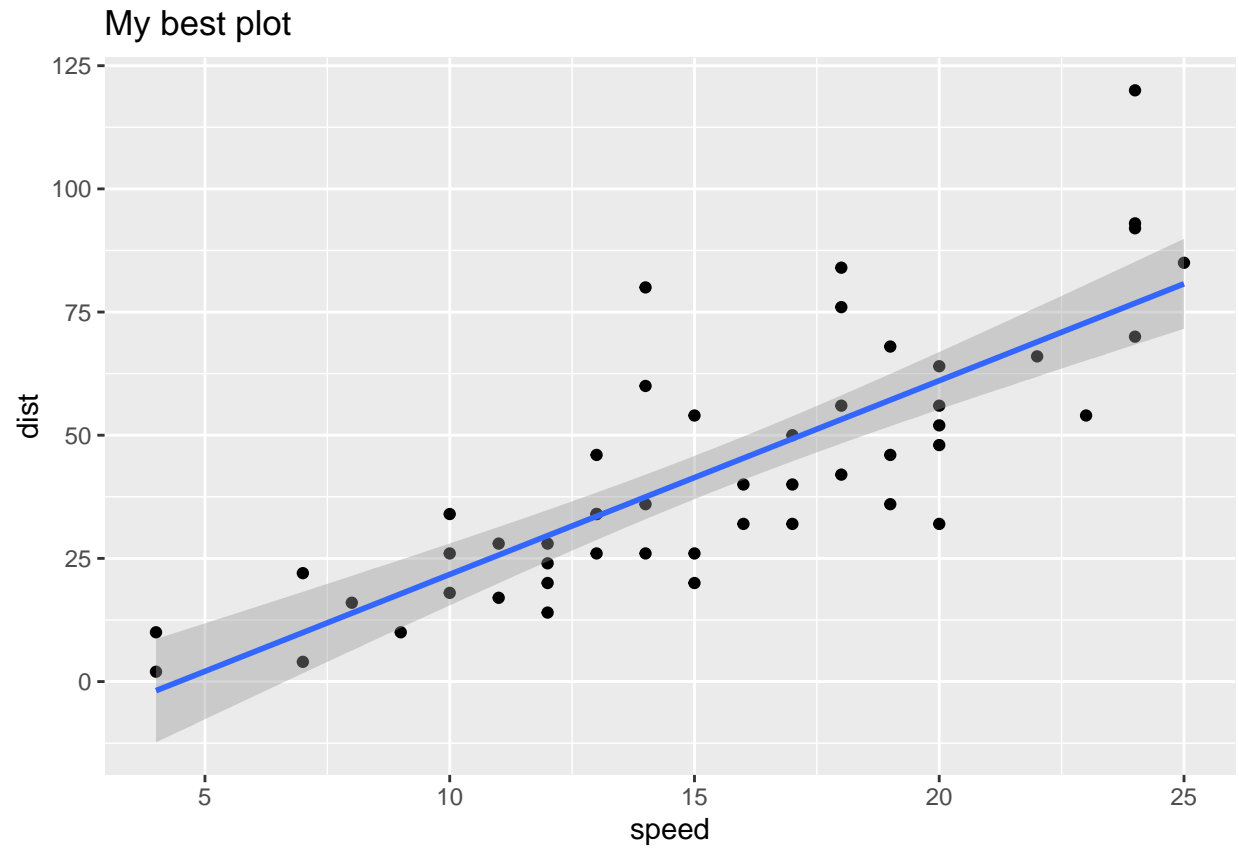


```
#every ggplot has a data + aes + geoms  
ggplot(data=cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth()  
  
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



```
#change to a linear model  
p <- ggplot(data=cars) + aes(x=speed, y=dist) + geom_point() + geom_smooth(method="lm")  
  
p + labs(title="My best plot")
```

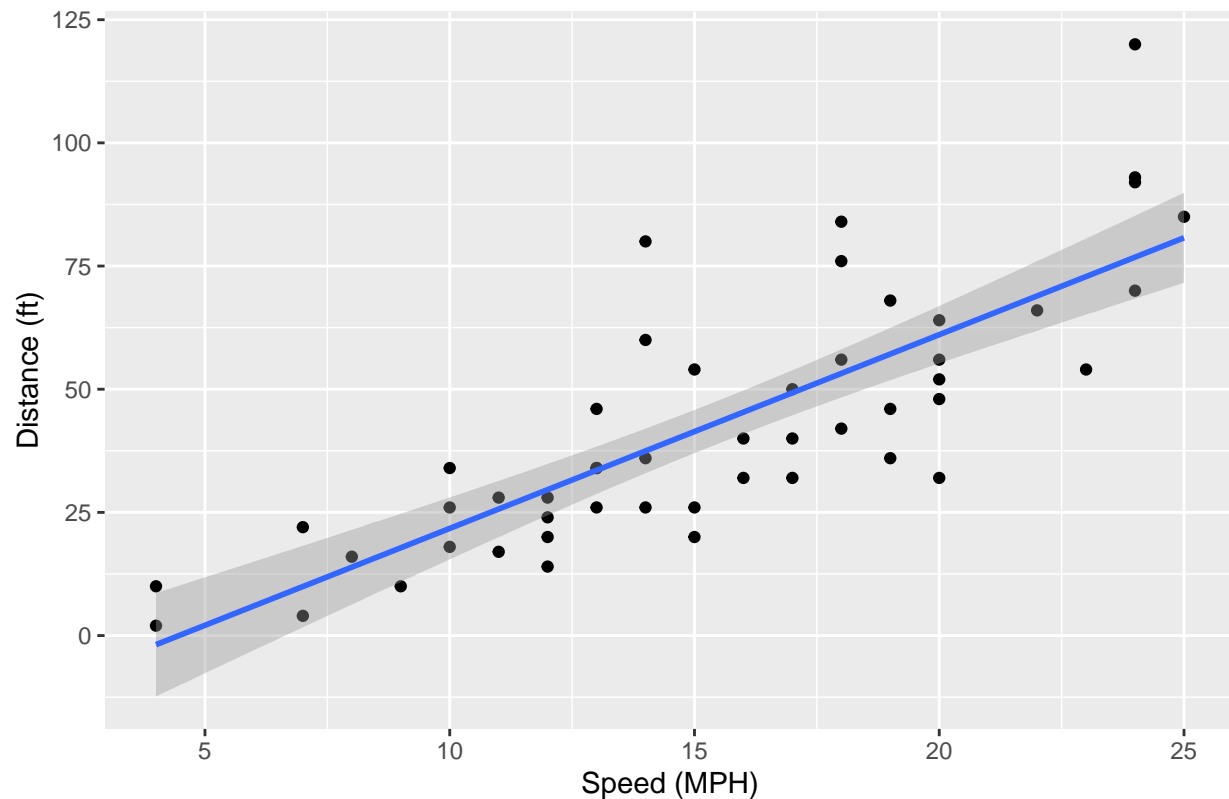
```
## 'geom_smooth()' using formula 'y ~ x'
```



```
p + labs(title="My best plot", x="Speed (MPH)", y="Distance (ft)")
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

My best plot



```
#Gene expression data
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

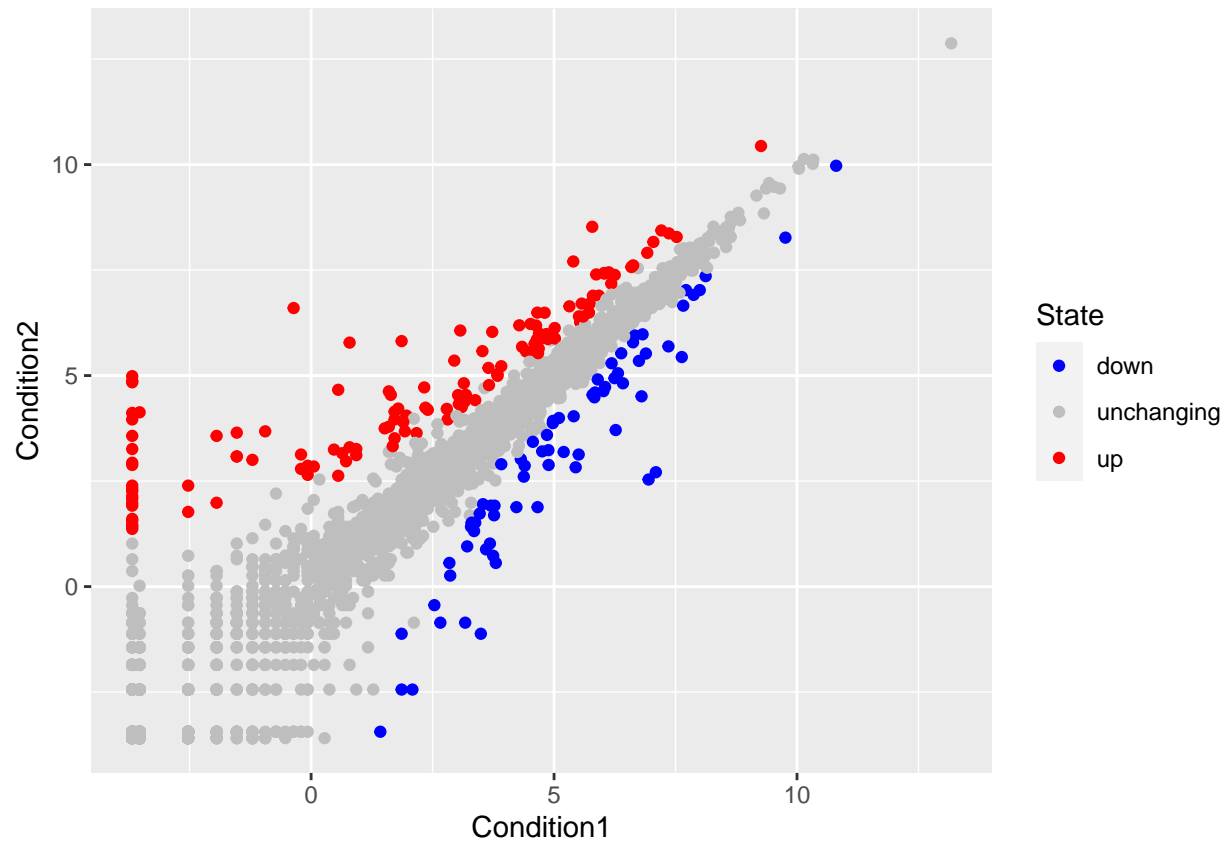
```
##      Gene Condition1 Condition2      State
## 1    A4GNT -3.6808610 -3.4401355  unchanging
## 2    AAAS  4.5479580  4.3864126  unchanging
## 3    AASDH  3.7190695  3.4787276  unchanging
## 4    AATF  5.0784720  5.0151916  unchanging
## 5    AATK  0.4711421  0.5598642  unchanging
## 6 AB015752.4 -3.6808610 -3.5921390  unchanging
```

```
#Q how to access one state
table( genes$State)
```

```
##
##      down unchanging      up
##      72      4997      127
```

```
#Making a scatterplot of the new data
p <- ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()
```

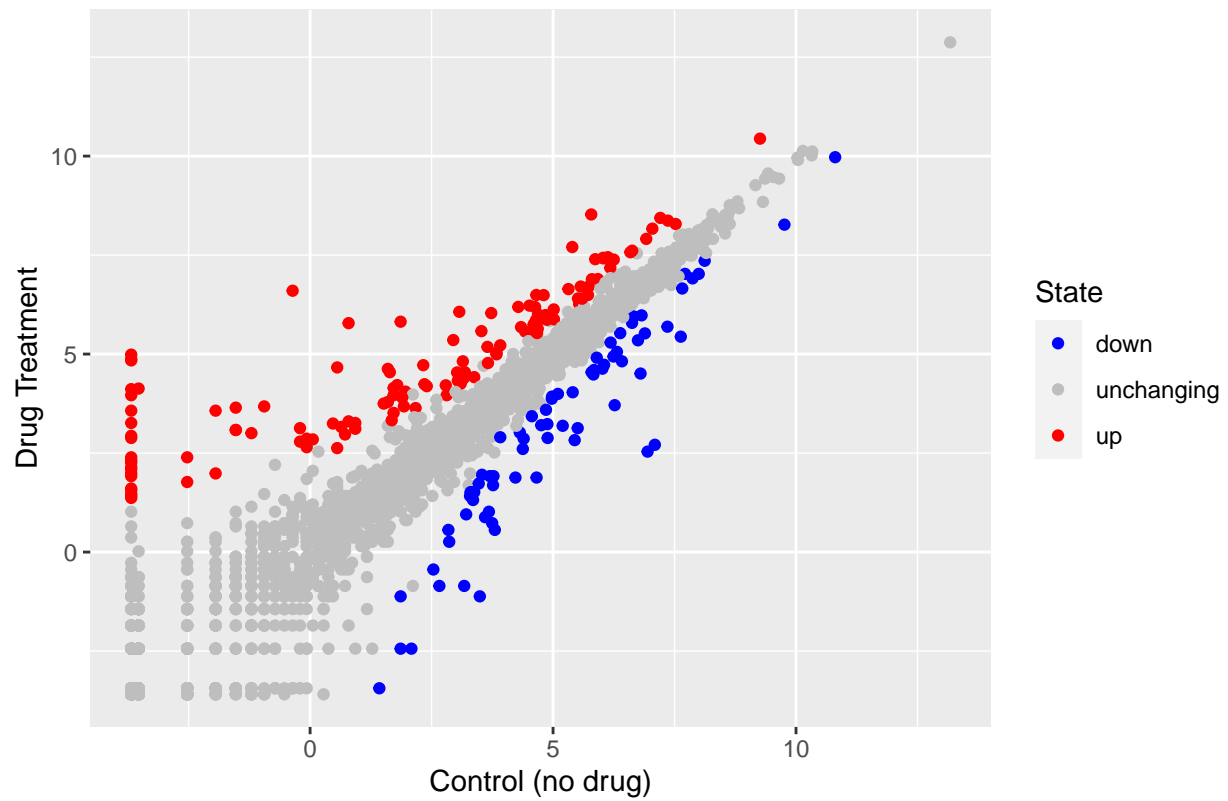
```
#Adding colors
p + scale_colour_manual( values=c("blue","gray","red") )
```



```
#Adding Labels
```

```
p + scale_colour_manual( values=c("blue","gray","red") ) + labs(title="Gene Expression Changes Upon Drug")
```

Gene Expression Changes Upon Drug Treatment



```
p + scale_colour_manual( values=c("light blue","gray","pink") ) + labs(title="Gene Expression Changes Upon Drug Treatment")
```

Gene Expression Changes Upon Drug Treatment

